

6. (Amended) The phosphoprotein (P) protein of Newcastle disease virus (NDV) encoded by the nucleic acid molecule of claim 3 or claim 4, wherein the protein comprises the amino acid sequence set forth as SEQ ID NO: 4.

15. (Amended) A fused or non-fused form of NDV nucleocapsid protein isolated and purified from culture of the transformed microorganism of claim 11 or claim 13, wherein the protein comprises the amino acid sequence set forth as SEQ ID NO: 3.

16. (Amended) A fused or non-fused form of NDV phosphoprotein isolated and purified from culture of the transformed microorganism of claim 12 or claim 14, wherein the protein comprises the amino acid set forth as SEQ ID NO: 4.

Remarks

Applicants have amended the claims and specification to include the sequence identification numbers for the sequences in the claims and have amended the claims for clarification. No new matter has been added by this amendment. Applicants also hereby request the entry of the sequence listing into the application.

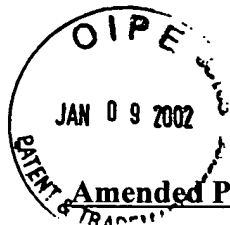
If the amendment is defective or unclear, the Examiner is invited to telephone the undersigned at the telephone number listed below.

Respectfully submitted,



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Amended Paragraphs of the Specification

Page 3, line 5.

NP coding region <(SEQ ID NO: 1)>

Page 5, line 3.

P gene coding region <(SEQ ID NO: 2)>

Page 6, line 19.

NP gene <(SEQ ID NO: 1)>: amino acid sequence <(SEQ ID NO: 3)>

Page 9, line 23.

P gene <(SEQ ID NO: 2)>: amino acid sequence <(SEQ ID NO: 4)>

Page 13, lines 11 through 18.

For the amplification of the NP gene

NPf1 (20 mer): 5'- cct tct gcc aac atg tct tc -3' (Forward primer<; SEQ ID NO: 5>)

NPr1 (20 mer): 5'- tca ata ccc cca gtc ggt gt -3' (Reverse primer<; SEQ ID NO: 6>)

NPr2 (18 mer): 5'- ata ccc cca gtc ggt gtc -3' (Reverse primer<; SEQ ID NO: 7>)

For the amplification of the P gene

Pf1 (20 mer): 5'- atg gcc acc ttt aca gat gc -3' (Forward primer<; SEQ ID NO: 8>)

Pr1 (23 mer): 5'- taa tta gcc att tag tgc aag gc -3' (Reverse primer<; SEQ ID NO: 9>)

Pr2 (21 mer): 5'- gcc att tag tgc aag gcg ctt -3' (Reverse primer<; SEQ ID NO: 10>)

Page 14, lines 13 through 27.

For the sequencing of the NP gene coding region

PTrcHis2F (21 mer): 5'- gag gta tat att aat gta tcg -3' <(SEQ ID NO: 11)>

SNPf1 (21 mer): 5'- gac tca tac atc agg aac acc -3' <(SEQ ID NO: 12)>

SNPf2 (21 mer): 5'- gat gag agc agt ggc gaa cag -3' <(SEQ ID NO: 13)>

PTrcHis2R (18 mer): 5'- gat tta atc tgt atc agg -3' <(SEQ ID NO: 14)>

SNPr1 (20 *mer*): 5'- tca ata ccc cca gtc ggt gt -3' <(SEQ ID NO: 15)>
 sNPr2 (21 *mer*): 5'- cta agt tgt aat acg tgg agc -3' <(SEQ ID NO: 16)>
 sNPr3 (21 *mer*): 5'- cca tcg atc tca aga aca tgc -3' <(SEQ ID NO: 17)>

For the sequencing of the P gene coding region

pTrcHis2F (21 *mer*): 5'- gag gta tat att aat gta tcg -3' <(SEQ ID NO: 18)>
 sPf1 (21 *mer*): 5'- gtc gac ttt gtg cag gcg atg -3' <(SEQ ID NO: 19)>
 sPf2 (21 *mer*): 5'- gga cac tgt ccg tgc att gat -3' <(SEQ ID NO: 20)>
 pTrcHis2.R (18 *mer*): 5'- gat tta atc tgt atc agg -3' <(SEQ ID NO: 21)>
 sPr1 (21 *mer*): 5'- cca ggg tcc aga att ttc atc -3' <(SEQ ID NO: 22)>
 sPr2 (22 *mer*): 5'- ggt gtg gat agc tgt ttg tct g -3' <(SEQ ID NO: 23)>

Amended Claims

1. (Amended) <A nucleic acid molecule>[Nucleotides] encoding the full length or part of the nucleocapsid (NP) protein of Newcastle disease virus (NDV).

2. (Amended) The [nucleotides as claimed in] <nucleic acid molecule of> claim 1<, wherein the nucleic acid molecule comprises the nucleotide sequence set forth as SEQ ID NO: 1.>

[characterised in that it has the following nucleotide sequence:

10	20	30	40	50	60
ATGTCTTCCG	TATTCGATGA	ATACGAGCAG	CTCCTCGCTG	CTCAGACTCG	CCCCAATGGA
70	80	90	100	110	120
GCTCACGGAG	GGGGAGAGAG	AGGGAGCACT	TTAAGAGTTG	AGGTCCCAGT	ATTCACTCTT
130	140	150	160	170	180
AACAGTGACG	ATCCAGAAGA	TAGATGGAAT	TTTGCGGTAT	TCTGTCTTCG	GATTGCTGTT
190	200	210	220	230	240
AGCGAGGACG	CCAACAAACC	GCTCAGGCAA	GGTGCTCTCA	TATCCCTCCT	GTGCTCCCAT
250	260	270	280	290	300
TCTCAAGTGA	TGAGGAACCA	TGTTGCCCTT	GCAGGAAAAC	AGAATGAGGC	TACTACTGACT
310	320	330	340	350	360
GTTCTTGAGA	TCGATGGTTT	TACCAGCAGC	GTGCCTCAGT	TCAACAACAG	GAGTGGGGTG
370	380	390	400	410	420

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TCTGAGGAGA GAGCACAGAG ATTCATGGTG ATAGCAGGGT CTCTCCCTCG GCGTGCAGT
      430      440      450      460      470      480
AACGGTACTC CGTTCGTCAC GGCTGGGGTT GAAGATGATG CACCAGAAGA TATCACTGAT
      490      500      510      520      530      540
ACTCTGGAAA GAATCCTGTC TATCCAGGCT CAGGTATGGG TCACAGTAGC GAAGGCCATG
      550      560      570      580      590      600
ACTGCATATG AGACAGCAGA TGAGTCGGAA ACAAGAAGAA TCAATAAGTA CATGCAGCAA
      610      620      630      640      650      660
GGCAGAGTCC AGAAGAAGTA CATCCTCCAC CCTGTATGCA GGAGTGCAAT TCAACTCACA
      670      680      690      700      710      720
ATCAGACATT CTCTGGCAGT CCGCATTTTC TTAGTTAGCG AGCTTAAGAG AGGCCGCAAT
      730      740      750      760      770      780
ACGGCAGGTG GGAGCTCCAC GTATTACAAC TTAGTAGGGG ATGTAGACTC ATACATCAGG
      790      800      810      820      830      840
AACACCGGAC TTACTGCATT CTTCTTACA CTCAAATATG GAATTAATAC CAAGACATCA
      850      860      870      880      890      900
GCCCTAGCAC TCAGCAGCCT CACAGGCGAT ATCCAAAAGA TGAAGCAGCT CATGCGTTTA
      910      920      930      940      950      960
TATCGGATGA AGGGAGAAAA TGCGCCGTAC ATGACATTGC TAGGTGACAG TGATCAGATG
      970      980      990      1000      1010      1020
AGCTTTGCAC CGGCTGAGTA TGCACAGCTT TATTCTTTTG CCATGGGCAT GGCATCAGTC
      1030      1040      1050      1060      1070      1080
TTAGATAAAG GAACTGGCAA ATACCAATTC GCCAGAGACT TCATGAGCAC ATCATTCTGG
      1090      1100      1110      1120      1130      1140
AGACTCGGGG TGGAGTATGC TCAGGCTCAG GGGAGTAGCA TCAACGAAGA CATGGCTGCT
      1150      1160      1170      1180      1190      1200
GAGCTAAAAC TAACCCCGGC AGCAAGAAGG GGCCTGGCAG CTGCTGCCCA ACGAGTGTCT
      1210      1220      1230      1240      1250      1260
GAGGAACTG GCAGCGTGGA TATTCCTACT CAACAAGCCG GGGTCCTCAC TGGGCTCAGC
      1270      1280      1290      1300      1310      1320
GATGGAGGCC CCCGAGCCTC TCAGGGTGGA TCGAACAAGT CGCAAGGGCA ACCAGATGCC
      1330      1340      1350      1360      1370      1380
GGAGATGGGG AGACCCAATT CTTGGATTTG ATGAGAGCAG TGGCGAACAG CATGCGAGAA
      1390      1400      1410      1420      1430      1440
GCGCCAAACT CCGCACAGAG CACCACCCAC CCGGAACCCC CCCCAGCTCC CGGGCCATCA
      1450      1460      1470      1480      1490      1500
CAAGATAACG ACACCGACTG GGGGTATTGA ..... ]

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3. (Amended) <A nucleic acid molecule>[Nucleotides] encoding the full length or part of the phosphoprotein (P) of Newcastle disease virus (NDV).
4. (Amended) The [nucleotides as claimed in]<nucleic acid molecule of> claim 3<, wherein the nucleic acid molecule comprises the nucleotide sequence set forth as SEQ ID NO: 2.> [characterised in that it has the following nucleotide sequence:

10	20	30	40	50	60
ATGGCCACCT	TTACAGATGC	GGAGATAGAT	GATATATTTG	AGACCAGTGG	AACTGTCATT
70	80	90	100	110	120
GACAGCATAA	TTACGGCCCA	GGGTAAATCA	GCAGAGACTG	TCGGAAGGAG	CGCAATCCCA
130	140	150	160	170	180
CAAGGCAAGA	CCAAAGCGCT	GAGCATAGCA	TGGGAGAAGC	ATGGGAGCAT	CCAACCATCC
190	200	210	220	230	240
ACCAGCCAGG	ACAACCCCGA	CCAACAGGAT	AGACCAGACA	AACAGCTATC	CACACCTGAG
250	260	270	280	290	300
CAGGCGACCC	CACACAACAG	CTCGCCAGCC	ACATCCGCCG	AACCGCTCCC	CACTCAGGCC
310	320	330	340	350	360
GCAGGTGAGG	CCGGCGACAC	ACAGCTCAAG	ACCGGAGCAA	GCAACTCTCT	TCTGTCTATG
370	380	390	400	410	420
CTCGACAAGC	TGAGCAATAA	ACCATCTAAT	GCTAAAAAGG	GCCCATGGTC	GAGTCCCCAG
430	440	450	460	470	480
GAAGGATATC	ATCAACCTCC	GACCCAACAA	CATGGGGATC	AGCCGAACCG	CGGAAACAGC
490	500	510	520	530	540
CAGGAGAGGC	TGCGGCACCA	AGCCAAGGCC	GCCCCTGGAA	GCCGGGGCAC	AGACGCGAGC
550	560	570	580	590	600
ACAGCATATC	ATGGACAATG	GAAGGAGTCA	CAACTATCAG	CTGGTGCAAC	CCCTCATGTG
610	620	630	640	650	660
CTCCAATCAG	GGCAGAGCCA	AGACAGTACT	CCTGTACCTG	TGGATCATGT	CCAGCCACCT
670	680	690	700	710	720
GTCGACTTTG	TGCAGGCGAT	GATGACTATG	ATGGAGGCGT	TATCACAGAA	GGTAAGTAAA
730	740	750	760	770	780
GTCGACTATC	AGCTAGACCT	AGTCTTAAAG	CAGACATCCT	CCATCCCTAT	GATGCGGTCT
790	800	810	820	830	840
GAAATCCAAC	AGCTAAAAAC	ATCTGTTGCG	GTCATGGAAG	CTAATTTAGG	CATGATGAAA
850	860	870	880	890	900

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ATTCTGGACC CTGGTTGTGC TAACATTTCA TCCTTAAGTG ATCTGCGGGC AGTCGCCCCG
          910          920          930          940          950          960
TCCCACCCAG TTTTAATTTT AGGCCCCCGA GATCCGTCCC CCTACGTGAC ACAAGGGGGT

          970          980          990          1000          1010          1020
GAGATGACAC TCAATAAACT CTCACAACCA GTACAACACC CTTCCGAGTT AATTAAATCT

          1030          1040          1050          1060          1070          1080
GCCACAGCGG GCGGACCTGA TATGGGAGTG GAAAAGGACA CTGTCCGTGC ATTGATCACC

          1090          1100          1110          1120          1130          1140
TCGCGCCCGA TGCATCCAAG CTCCTCAGCT AAGCTCCTGA GTAAGCTGGA TGCAGCCGGG

          1150          1160          1170          1180          1190          1200
TCGATTGAAG AGATCAGAAA GATCAAGCGC CTTGCACTAA ATGGCTAA... ..]

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5. (Amended) [The]<A nucleocapsid (NP)> protein <of Newcastle disease virus (NDV) encoded by the nucleic acid molecule>[coded according to] <of> claim 1 or claim 2<, wherein the protein comprises the amino acid sequence set forth as SEQ ID NO: 3.> [characterised in that it has the following amino acid sequence:

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1  M  S  S  V  F  D  E  Y  E  Q  L  L  A  A  Q  T      16
   ATG TCT TCC GTA TTC GAT GAA TAC GAG CAG CTC CTC GCT GCT CAG ACT
   1          10          20          30          40

17 R  P  N  G  A  H  G  G  G  E  R  G  S  T  L  R      32
   CGC CCC AAT GGA GCT CAC GGA GGG GGA GAG AGA GGG AGC ACT TTA AGA
   50          60          70          80          90

33 V  E  V  P  V  F  T  L  N  S  D  D  P  E  D  R      48
   GTT GAG GTC CCA GTA TTC ACT CTT AAC AGT GAC GAT CCA GAA GAT AGA
   100         110         120         130         140

49 W  N  F  A  V  F  C  L  R  I  A  V  S  E  D  A      64
   TGG AAT TTT GCG GTA TTC TGT CTT CGG ATT GCT GTT AGC GAG GAC GCC
   150         160         170         180         190

65 N  K  P  L  R  Q  G  A  L  I  S  L  L  C  S  H      80
   AAC AAA CCG CTC AGG CAA GGT GCT CTC ATA TCC CTC CTG TGC TCC CAT
   200         210         220         230         240

81 S  Q  V  M  R  N  H  V  A  L  A  G  K  Q  N  E      96
   TCT CAA GTG ATG AGG AAC CAT GTT GCC CTT GCA GGA AAA CAG AAT GAG
   250         260         270         280

97 A  T  L  T  V  L  E  I  D  G  F  T  S  S  V  P     112
   GCT ACA CTG ACT GTT CTT GAG ATC GAT GGT TTT ACC AGC AGC GTG CCT
   290         300         310         320         330

113 Q  F  N  N  R  S  G  V  S  E  E  R  A  Q  R  F     128
   CAG TTC AAC AAC AGG AGT GGG GTG TCT GAG GAG AGA GCA CAG AGA TTC
   340         350         360         370         380

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129	M	V	I	A	G	S	L	P	R	A	C	S	N	G	T	P	144
	ATG	GTG	ATA	GCA	GGG	TCT	CTC	CCT	CGG	GCG	TGC	AGT	AAC	GGT	ACT	CCG	
	390				400			410				420			430		
145	F	V	T	A	G	V	E	D	D	A	P	E	D	I	T	D	160
	TTC	GTC	ACG	GCT	GGG	GTT	GAA	GAT	GAT	GCA	CCA	GAA	GAT	ATC	ACT	GAT	
	440				450			460				470			480		
161	T	L	E	R	I	L	S	I	Q	A	Q	V	W	V	T	V	176
	ACT	CTG	GAA	AGA	ATC	CTG	TCT	ATC	CAG	GCT	CAG	GTA	TGG	GTC	ACA	GTA	
	490				500			510				520					
177	A	K	A	M	T	A	Y	E	T	A	D	E	S	E	T	R	192
	GCG	AAG	GCC	ATG	ACT	GCA	TAT	GAG	ACA	GCA	GAT	GAG	TCG	GAA	ACA	AGA	
	530			540			550			560			570				
193	R	I	N	K	Y	M	Q	Q	G	R	V	Q	K	K	Y	I	208
	AGA	ATC	AAT	AAG	TAC	ATG	CAG	CAA	GGC	AGA	GTC	CAG	AAG	AAG	TAC	ATC	
	580			590			600			610			620				
209	L	H	P	V	C	R	S	A	I	Q	L	T	I	R	H	S	224
	CTC	CAC	CCT	GTA	TGC	AGG	AGT	GCA	ATT	CAA	CTC	ACA	ATC	AGA	CAT	TCT	
	630			640			650			660			670				
225	L	A	V	R	I	F	L	V	S	E	L	K	R	G	R	N	240
	CTG	GCA	GTC	CGC	ATT	TTC	TTA	GTT	AGC	GAG	CTT	AAG	AGA	GGC	CGC	AAT	
	680			690			700			710			720				
241	T	A	G	G	S	S	T	Y	Y	N	L	V	G	D	V	D	256
	ACG	GCA	GGT	GGG	AGC	TCC	ACG	TAT	TAC	AAC	TTA	GTA	GGG	GAT	GTA	GAC	
	730			740			750			760							
257	S	Y	I	R	N	T	G	L	T	A	F	F	L	T	L	K	272
	TCA	TAC	ATC	AGG	AAC	ACC	GGA	CTT	ACT	GCA	TTC	TTC	CTT	ACA	CTC	AAA	
	770			780			790			800			810				
273	Y	G	I	N	T	K	T	S	A	L	A	L	S	S	L	T	288
	TAT	GGA	ATT	AAT	ACC	AAG	ACA	TCA	GCC	CTA	GCA	CTC	AGC	AGC	CTC	ACA	
	820			830			840			850			860				
289	G	D	I	Q	K	M	K	Q	L	M	R	L	Y	R	M	K	304
	GGC	GAT	ATC	CAA	AAG	ATG	AAG	CAG	CTC	ATG	CGT	TTA	TAT	CGG	ATG	AAG	
	870			880			890			900			910				
305	G	E	N	A	P	Y	M	T	L	L	G	D	S	D	Q	M	320
	GGA	GAA	AAT	GCG	CCG	TAC	ATG	ACA	TTG	CTA	GGT	GAC	AGT	GAT	CAG	ATG	
	920			930			940			950			960				
321	S	F	A	P	A	E	Y	A	Q	L	Y	S	F	A	M	G	336
	AGC	TTT	GCA	CCG	GCT	GAG	TAT	GCA	CAG	CTT	TAT	TCT	TTT	GCC	ATG	GGC	
	970			980			990			1000							
337	M	A	S	V	L	D	K	G	T	G	K	Y	Q	F	A	R	352
	ATG	GCA	TCA	GTC	TTA	GAT	AAA	GGA	ACT	GGC	AAA	TAC	CAA	TTC	GCC	AGA	
	1010			1020			1030			1040			1050				
353	D	F	M	S	T	S	F	W	R	L	G	V	E	Y	A	Q	368
	GAC	TTC	ATG	AGC	ACA	TCA	TTC	TGG	AGA	CTC	GGG	GTG	GAG	TAT	GCT	CAG	
	1060			1070			1080			1090			1100				
369	A	Q	G	S	S	I	N	E	D	M	A	A	E	L	K	L	384
	GCT	CAG	GGG	AGT	AGC	ATC	AAC	GAA	GAC	ATG	GCT	GCT	GAG	CTA	AAA	CTA	
	1110			1120			1130			1140			1150				

385	T	P	A	A	R	R	G	L	A	A	A	A	Q	R	V	S	400
	ACC	CCG	GCA	GCA	AGA	AGG	GGC	CTG	GCA	GCT	GCT	GCC	CAA	CGA	GTG	TCT	
			1160			1170			1180			1190			1200		
401	E	E	T	G	S	V	D	I	P	T	Q	Q	A	G	V	L	416
	GAG	GAA	ACT	GGC	AGC	GTG	GAT	ATT	CCT	ACT	CAA	CAA	GCC	GGG	GTC	CTC	
			1210			1220			1230			1240					
417	T	G	L	S	D	G	G	P	R	A	S	Q	G	G	S	N	432
	ACT	GGG	CTC	AGC	GAT	GGA	GGC	CCC	CGA	GCC	TCT	CAG	GGT	GGA	TCG	AAC	
	1250			1260			1270			1280			1290				
433	K	S	Q	G	Q	P	D	A	G	D	G	E	T	Q	F	L	448
	AAG	TCG	CAA	GGG	CAA	CCA	GAT	GCC	GGA	GAT	GGG	GAG	ACC	CAA	TTC	TTG	
	1300			1310			1320			1330			1340				
449	D	L	M	R	A	V	A	N	S	M	R	E	A	P	N	S	464
	GAT	TTG	ATG	AGA	GCA	GTG	GCG	AAC	AGC	ATG	CGA	GAA	GCG	CCA	AAC	TCC	
	1350			1360			1370			1380			1390				
465	A	Q	S	T	T	H	P	E	P	P	P	T	P	G	P	S	480
	GCA	CAG	AGC	ACC	ACC	CAC	CCG	GAA	CCC	CCC	CCG	ACT	CCC	GGG	CCA	TCC	
		1400			1410			1420			1430			1440			
481	Q	D	N	D	T	D	W	G	Y	*							490
	CAA	GAT	AAC	GAC	ACC	GAC	TGG	GGG	TAT	TGA							
			1450			1460			1470]

6. (Amended) [The] <A phosphoprotein (P)> protein <of Newcastle disease virus (DNV) encoded by the nucleic acid molecule> [coded according to] <of> claim 3 or claim 4<, wherein the protein comprises the amino acid sequence set forth as SEQ ID NO: 4.> [characterised in that it has the following amino acid sequence:

1	M	A	T	F	T	D	A	E	I	D	D	I	F	E	T	S	16
	ATG	GCC	ACC	TTT	ACA	GAT	GCG	GAG	ATA	GAT	GAT	ATA	TTT	GAG	ACC	AGT	
	1			10			20			30			40				
17	G	T	V	I	D	S	I	I	T	A	Q	G	K	S	A	E	32
	GGA	ACT	GTC	ATT	GAC	AGC	ATA	ATT	ACG	GCC	CAG	GGT	AAA	TCA	GCA	GAG	
	50			60			70			80			90				
33	T	V	G	R	S	A	I	P	Q	G	K	T	K	A	L	S	48
	ACT	GTC	GGA	AGG	AGC	GCA	ATC	CCA	CAA	GGC	AAG	ACC	AAA	GCG	CTG	AGC	
	100			110			120			130			140				
49	I	A	W	E	K	H	G	S	I	Q	P	S	T	S	Q	D	64
	ATA	GCA	TGG	GAG	AAG	CAT	GGG	AGC	ATC	CAA	CCA	TCC	ACC	AGC	CAG	GAC	
	150			160			170			180			190				
65	N	P	D	Q	Q	D	R	P	D	K	Q	L	S	T	P	E	80
	AAC	CCC	GAC	CAA	CAG	GAT	AGA	CCA	GAC	AAA	CAG	CTA	TCC	ACA	CCT	GAG	
		200			210			220			230			240			
81	Q	A	T	P	H	N	S	S	P	A	T	S	A	E	P	L	96
	CAG	GCG	ACC	CCA	CAC	AAC	AGC	TCG	CCA	GCC	ACA	TCC	GCC	GAA	CCG	CTC	
		250			260			270			280						

97	P	T	Q	A	A	G	E	A	G	D	T	Q	L	K	T	G	112
	CCC	ACT	CAG	GCC	GCA	GGT	GAG	GCC	GGC	GAC	ACA	CAG	CTC	AAG	ACC	GGA	
	290			300			310			320			330				
113	A	S	N	S	L	L	S	M	L	D	K	L	S	N	K	P	128
	GCA	AGC	AAC	TCT	CTT	CTG	TCT	ATG	CTC	GAC	AAG	CTG	AGC	AAT	AAA	CCA	
	340			350			360			370			380				
129	S	N	A	K	K	G	P	W	S	S	P	Q	E	G	Y	H	144
	TCT	AAT	GCT	AAA	AAG	GGC	CCA	TGG	TCG	AGT	CCC	CAG	GAA	GGA	TAT	CAT	
	390			400			410			420			430				
145	Q	P	P	T	Q	Q	H	G	D	Q	P	N	R	G	N	S	160
	CAA	CCT	CCG	ACC	CAA	CAA	CAT	GGG	GAT	CAG	CCG	AAC	CGC	GGA	AAC	AGC	
	440			450			460			470			480				
161	Q	E	R	L	R	H	Q	A	K	A	A	P	G	S	R	G	176
	CAG	GAG	AGG	CTG	CGG	CAC	CAA	GCC	AAG	GCC	GCC	CCT	GGA	AGC	CGG	GGC	
	490			500			510			520			530				
177	T	D	A	S	T	A	Y	H	G	Q	W	K	E	S	Q	L	192
	ACA	GAC	GCG	AGC	ACA	GCA	TAT	CAT	GGA	CAA	TGG	AAG	GAG	TCA	CAA	CTA	
	530			540			550			560			570				
193	S	A	G	A	T	P	H	V	L	Q	S	G	Q	S	Q	D	208
	TCA	GCT	GGT	GCA	ACC	CCT	CAT	GTG	CTC	CAA	TCA	GGG	CAG	AGC	CAA	GAC	
	580			590			600			610			620				
209	S	T	P	V	P	V	D	H	V	Q	P	P	V	D	F	V	224
	AGT	ACT	CCT	GTA	CCT	GTG	GAT	CAT	GTC	CAG	CCA	CCT	GTC	GAC	TTT	GTG	
	630			640			650			660			670				
225	Q	A	M	M	T	M	M	E	A	L	S	Q	K	V	S	K	240
	CAG	GCG	ATG	ATG	ACT	ATG	ATG	GAG	GCG	TTA	TCA	CAG	AAG	GTA	AGT	AAA	
	680			690			700			710			720				
241	V	D	Y	Q	L	D	L	V	L	K	Q	T	S	S	I	P	256
	GTC	GAC	TAT	CAG	CTA	GAC	CTA	GTC	TTA	AAG	CAG	ACA	TCC	TCC	ATC	CCT	
	730			740			750			760			770				
257	M	M	R	S	E	I	Q	Q	L	K	T	S	V	A	V	M	272
	ATG	ATG	CGG	TCT	GAA	ATC	CAA	CAG	CTA	AAA	ACA	TCT	GTT	GCG	GTC	ATG	
	770			780			790			800			810				
273	E	A	N	L	G	M	M	K	I	L	D	P	G	C	A	N	288
	GAA	GCT	AAT	TTA	GGC	ATG	ATG	AAA	ATT	CTG	GAC	CCT	GGT	TGT	GCT	AAC	
	820			830			840			850			860				
289	I	S	S	L	S	D	L	R	A	V	A	R	S	H	P	V	304
	ATT	TCA	TCC	TTA	AGT	GAT	CTG	CGG	GCA	GTC	GCC	CGG	TCC	CAC	CCA	GTT	
	870			880			890			900			910				
305	L	I	S	G	P	G	D	P	S	P	Y	V	T	Q	G	G	320
	TTA	ATT	TCA	GGC	CCC	GGA	GAT	CCG	TCC	CCC	TAC	GTG	ACA	CAA	GGG	GGT	
	920			930			940			950			960				
321	E	M	T	L	N	K	L	S	Q	P	V	Q	H	P	S	E	336
	GAG	ATG	ACA	CTC	AAT	AAA	CTC	TCA	CAA	CCA	GTA	CAA	CAC	CCT	TCC	GAG	
	970			980			990			1000							
337	L	I	K	S	A	T	A	G	G	P	D	M	G	V	E	K	352
	TTA	ATT	AAA	TCT	GCC	ACA	GCG	GGC	GGA	CCT	GAT	ATG	GGA	GTG	GAA	AAG	

	1010	1020	1030	1040	1050	
353	D T V R A L I T S R P M H P S S					368
	GAC ACT GTC CGT GCA TTG ATC ACC TCG CGC CCG ATG CAT CCA AGC TCC					
	1060	1070	1080	1090	1100	
369	S A K L L S K L D A A G S I E E					384
	TCA GCT AAG CTC CTG AGT AAG CTG GAT GCA GCC GGG TCG ATT GAA GAG					
	1110	1120	1130	1140	1150	
385	I R K I K R L A L N G *					396
	ATC AGA AAG ATC AAG CGC CTT GCA CTA AAT GGC TAA					
	1160	1170	1180]

15. (Amended) A fused or non-fused form of NDV nucleocapsid protein isolated and purified from culture of the transformed microorganism of claim 11 or claim 13<, wherein the protein comprises the amino acid sequence set forth as SEQ ID NO: 3.> [characterised in that it has the following amino acid sequence:

1	M S S V F D E Y E Q L L A A Q T	16
	ATG TCT TCC GTA TTC GAT GAA TAC GAG CAG CTC CTC GCT GCT CAG ACT	
	1 10 20 30 40	
17	R P N G A H G G G E R G S T L R	32
	CGC CCC AAT GGA GCT CAC GGA GGG GGA GAG AGA GGG AGC ACT TTA AGA	
	50 60 70 80 90	
33	V E V P V F T L N S D D P E D R	48
	GTT GAG GTC CCA GTA TTC ACT CTT AAC AGT GAC GAT CCA GAA GAT AGA	
	100 110 120 130 140	
49	W N F A V F C L R I A V S E D A	64
	TGG AAT TTT GCG GTA TTC TGT CTT CGG ATT GCT GTT AGC GAG GAC GCC	
	150 160 170 180 190	
65	N K P L R Q G A L I S L L C S H	80
	AAC AAA CCG CTC AGG CAA GGT GCT CTC ATA TCC CTC CTG TGC TCC CAT	
	200 210 220 230 240	
81	S Q V M R N H V A L A G K Q N E	96
	TCT CAA GTG ATG AGG AAC CAT GTT GCC CTT GCA GGA AAA CAG AAT GAG	
	250 260 270 280	
97	A T L T V L E I D G F T S S V P	112
	GCT ACA CTG ACT GTT CTT GAG ATC GAT GGT TTT ACC AGC AGC GTG CCT	
	290 300 310 320 330	
113	Q F N N R S G V S E E R A Q R F	128
	CAG TTC AAC AAC AGG AGT GGG GTG TCT GAG GAG AGA GCA CAG AGA TTC	
	340 350 360 370 380	
129	M V I A G S L P R A C S N G T P	144
	ATG GTG ATA GCA GGG TCT CTC CCT CGG GCG TGC AGT AAC GGT ACT CCG	
	390 400 410 420 430	
145	F V T A G V E D D A P E D I T D	160
	TTC GTC ACG GCT GGG GTT GAA GAT GAT GCA CCA GAA GAT ATC ACT GAT	

	440	450	460	470	480	
161	T L E R I L S I Q A Q V W V T V					176
	ACT CTG GAA AGA ATC CTG TCT ATC CAG GCT CAG GTA TGG GTC ACA GTA					
	490	500	510	520		
177	A K A M T A Y E T A D E S E T R					192
	GCG AAG GCC ATG ACT GCA TAT GAG ACA GCA GAT GAG TCG GAA ACA AGA					
	530	540	550	560	570	
193	R I N K Y M Q Q G R V Q K K Y I					208
	AGA ATC AAT AAG TAC ATG CAG CAA GGC AGA GTC CAG AAG AAG TAC ATC					
	580	590	600	610	620	
209	L H P V C R S A I Q L T I R H S					224
	CTC CAC CCT GTA TGC AGG AGT GCA ATT CAA CTC ACA ATC AGA CAT TCT					
	630	640	650	660	670	
225	L A V R I F L V S E L K R G R N					240
	CTG GCA GTC CGC ATT TTC TTA GTT AGC GAG CTT AAG AGA GGC CGC AAT					
	680	690	700	710	720	
241	T A G G S S T Y Y N L V G D V D					256
	ACG GCA GGT GGG AGC TCC ACG TAT TAC AAC TTA GTA GGG GAT GTA GAC					
	730	740	750	760		
257	S Y I R N T G L T A F F L T L K					272
	TCA TAC ATC AGG AAC ACC GGA CTT ACT GCA TTC TTC CTT ACA CTC AAA					
	770	780	790	800	810	
273	Y G I N T K T S A L A L S S L T					288
	TAT GGA ATT AAT ACC AAG ACA TCA GCC CTA GCA CTC AGC AGC CTC ACA					
	820	830	840	850	860	
289	G D I Q K M K Q L M R L Y R M K					304
	GGC GAT ATC CAA AAG ATG AAG CAG CTC ATG CGT TTA TAT CGG ATG AAG					
	870	880	890	900	910	
305	G E N A P Y M T L L G D S D Q M					320
	GGA GAA AAT GCG CCG TAC ATG ACA TTG CTA GGT GAC AGT GAT CAG ATG					
	920	930	940	950	960	
321	S F A P A E Y A Q L Y S F A M G					336
	AGC TTT GCA CCG GCT GAG TAT GCA CAG CTT TAT TCT TTT GCC ATG GGC					
	970	980	990	1000		
337	M A S V L D K G T G K Y Q F A R					352
	ATG GCA TCA GTC TTA GAT AAA GGA ACT GGC AAA TAC CAA TTC GCC AGA					
	1010	1020	1030	1040	1050	
353	D F M S T S F W R L G V E Y A Q					368
	GAC TTC ATG AGC ACA TCA TTC TGG AGA CTC GGG GTG GAG TAT GCT CAG					
	1060	1070	1080	1090	1100	
369	A Q G S S I N E D M A A E L K L					384
	GCT CAG GGG AGT AGC ATC AAC GAA GAC ATG GCT GCT GAG CTA AAA CTA					
	1110	1120	1130	1140	1150	
385	T P A A R R G L A A A A Q R V S					400
	ACC CCG GCA GCA AGA AGG GGC CTG GCA GCT GCT GCC CAA CGA GTG TCT					
	1160	1170	1180	1190	1200	
401	E E T G S V D I P T Q Q A G V L					416

	GAG	GAA	ACT	GGC	AGC	GTG	GAT	ATT	CCT	ACT	CAA	CAA	GCC	GGG	GTC	CTC	
			1210			1220			1230				1240				
417	T	G	L	S	D	G	G	P	R	A	S	Q	G	G	S	N	432
	ACT	GGG	CTC	AGC	GAT	GGA	GGC	CCC	CGA	GCC	TCT	CAG	GGT	GGA	TCG	AAC	
	1250		1260			1270			1280			1290					
433	K	S	Q	G	Q	P	D	A	G	D	G	E	T	Q	F	L	448
	AAG	TCG	CAA	GGG	CAA	CCA	GAT	GCC	GGA	GAT	GGG	GAG	ACC	CAA	TTC	TTG	
	1300		1310			1320			1330			1340					
449	D	L	M	R	A	V	A	N	S	M	R	E	A	P	N	S	464
	GAT	TTG	ATG	AGA	GCA	GTG	GCG	AAC	AGC	ATG	CGA	GAA	GCG	CCA	AAC	TCC	
	1350		1360			1370			1380			1390					
465	A	Q	S	T	T	H	P	E	P	P	P	T	P	G	P	S	480
	GCA	CAG	AGC	ACC	ACC	CAC	CCG	GAA	CCC	CCC	CCG	ACT	CCC	GGG	CCA	TCC	
	1400		1410			1420			1430			1440					
481	Q	D	N	D	T	D	W	G	Y	*							490
	CAA	GAT	AAC	GAC	ACC	GAC	TGG	GGG	TAT	TGA							
		1450		1460		1470]

16. (Amended) A fused or non-fused form of NDV phosphoprotein isolated and purified from culture of the transformed microorganism of claim 12 or claim 14<, wherein the protein comprises the amino acid sequence set forth as SEQ ID NO: 4.> [characterised in that it has the following amino acid sequence:

1	M	A	T	F	T	D	A	E	I	D	D	I	F	E	T	S	16
	ATG	GCC	ACC	TTT	ACA	GAT	GCG	GAG	ATA	GAT	GAT	ATA	TTT	GAG	ACC	AGT	
	1		10			20			30			40					
17	G	T	V	I	D	S	I	I	T	A	Q	G	K	S	A	E	32
	GGA	ACT	GTC	ATT	GAC	AGC	ATA	ATT	ACG	GCC	CAG	GGT	AAA	TCA	GCA	GAG	
	50		60			70			80			90					
33	T	V	G	R	S	A	I	P	Q	G	K	T	K	A	L	S	48
	ACT	GTC	GGA	AGG	AGC	GCA	ATC	CCA	CAA	GGC	AAG	ACC	AAA	GCG	CTG	AGC	
	100		110			120			130			140					
49	I	A	W	E	K	H	G	S	I	Q	P	S	T	S	Q	D	64
	ATA	GCA	TGG	GAG	AAG	CAT	GGG	AGC	ATC	CAA	CCA	TCC	ACC	AGC	CAG	GAC	
	150		160			170			180			190					
65	N	P	D	Q	Q	D	R	P	D	K	Q	L	S	T	P	E	80
	AAC	CCC	GAC	CAA	CAG	GAT	AGA	CCA	GAC	AAA	CAG	CTA	TCC	ACA	CCT	GAG	
	200		210			220			230			240					
81	Q	A	T	P	H	N	S	S	P	A	T	S	A	E	P	L	96
	CAG	GCG	ACC	CCA	CAC	AAC	AGC	TCG	CCA	GCC	ACA	TCC	GCC	GAA	CCG	CTC	
		250		260		270			280								
97	P	T	Q	A	A	G	E	A	G	D	T	Q	L	K	T	G	112
	CCC	ACT	CAG	GCC	GCA	GGT	GAG	GCC	GGC	GAC	ACA	CAG	CTC	AAG	ACC	GGA	
	290		300			310			320			330					

113	A S N S L L S M L D K L S N K P	128
	GCA AGC AAC TCT CTT CTG TCT ATG CTC GAC AAG CTG AGC AAT AAA CCA	
	340 350 360 370 380	
129	S N A K K G P W S S P Q E G Y H	144
	TCT AAT GCT AAA AAG GGC CCA TGG TCG AGT CCC CAG GAA GGA TAT CAT	
	390 400 410 420 430	
145	Q P P T Q Q H G D Q P N R G N S	160
	CAA CCT CCG ACC CAA CAA CAT GGG GAT CAG CCG AAC CGC GGA AAC AGC	
	440 450 460 470 480	
161	Q E R L R H Q A K A A P G S R G	176
	CAG GAG AGG CTG CGG CAC CAA GCC AAG GCC GCC CCT GGA AGC CGG GGC	
	490 500 510 520	
177	T D A S T A Y H G Q W K E S Q L	192
	ACA GAC GCG AGC ACA GCA TAT CAT GGA CAA TGG AAG GAG TCA CAA CTA	
	530 540 550 560 570	
193	S A G A T P H V L Q S G Q S Q D	208
	TCA GCT GGT GCA ACC CCT CAT GTG CTC CAA TCA GGG CAG AGC CAA GAC	
	580 590 600 610 620	
209	S T P V P V D H V Q P P V D F V	224
	AGT ACT CCT GTA CCT GTG GAT CAT GTC CAG CCA CCT GTC GAC TTT GTG	
	630 640 650 660 670	
225	Q A M M T M M E A L S Q K V S K	240
	CAG GCG ATG ATG ACT ATG ATG GAG GCG TTA TCA CAG AAG GTA AGT AAA	
	680 690 700 710 720	
241	V D Y Q L D L V L K Q T S S I P	256
	GTC GAC TAT CAG CTA GAC CTA GTC TTA AAG CAG ACA TCC TCC ATC CCT	
	730 740 750 760	
257	M M R S E I Q Q L K T S V A V M	272
	ATG ATG CCG TCT GAA ATC CAA CAG CTA AAA ACA TCT GTT GCG GTC ATG	
	770 780 790 800 810	
273	E A N L G M M K I L D P G C A N	288
	GAA GCT AAT TTA GGC ATG ATG AAA ATT CTG GAC CCT GGT TGT GCT AAC	
	820 830 840 850 860	
289	I S S L S D L R A V A R S H P V	304
	ATT TCA TCC TTA AGT GAT CTG CGG GCA GTC GCC CGG TCC CAC CCA GTT	
	870 880 890 900 910	
305	L I S G P G D P S P Y V T Q G G	320
	TTA ATT TCA GGC CCC GGA GAT CCG TCC CCC TAC GTG ACA CAA GGG GGT	
	920 930 940 950 960	
321	E M T L N K L S Q P V Q H P S E	336
	GAG ATG ACA CTC AAT AAA CTC TCA CAA CCA GTA CAA CAC CCT TCC GAG	
	970 980 990 1000	
337	L I K S A T A G G P D M G V E K	352
	TTA ATT AAA TCT GCC ACA GCG GGC GGA CCT GAT ATG GGA GTG GAA AAG	
	1010 1020 1030 1040 1050	
353	D T V R A L I T S R P M H P S S	368
	GAC ACT GTC CGT GCA TTG ATC ACC TCG CGC CCG ATG CAT CCA AGC TCC	

	1060			1070			1080			1090			1100				
369	S	A	K	L	L	S	K	L	D	A	A	G	S	I	E	E	384
	TCA	GCT	AAG	CTC	CTG	AGT	AAG	CTG	GAT	GCA	GCC	GGG	TCG	ATT	GAA	GAG	
	1110			1120			1130			1140			1150				
385	I	R	K	I	K	R	L	A	L	N	G	*					396
	ATC	AGA	AAG	ATC	AAG	CGC	CTT	GCA	CTA	AAT	GGC	TAA					
	1160			1170			1180										